

GenCore version 5.1.7
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 OM protein - protein search, using sw model
 Run on: April 17, 2006, 15:24:29 ; Search time 237 Seconds
 (without alignments)
 256.014 Million cell updates/sec
 Title: US-10-027-603-2_COPY_20_105
 Perfect score: 86
 Sequence: 1 AVITACERDVQCGAGTCCA.....CSRFPDGRYCRSMDLKNINF 86

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0
 Searched: 2166443 seqs, 705528306 residues
 Word size : 1
 Total number of hits satisfying chosen parameters: 2166443
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Listing first 45 summaries
 Database : UniProt 05.80: *
 1: uniprot_sprot: *
 2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	86	100.0	105	1 PROK1_HUMAN	P58294 homo sapien
2	86	100.0	105	2 Q5VWD4_HUMAN	Q5VWD4 homo sapien
3	47	54.7	105	2 Q8TC69_HUMAN	Q8TC69 homo sapien
4	29	33.7	105	1 PROK1_RAT	Q8r414 rattus norv
5	18	20.9	81	2 Q8K457_MOUSE	Q8K457 mus musculus
6	10	11.6	81	1 VPRA_DENPO	P25687 dendroaspis
7	10	11.6	102	2 Q4SR12_TETNG	Q4sr12 tetraodon n
8	8	9.3	88	2 Q5D228_HADSP	Q5D228 hadronyche
9	8	9.3	88	2 Q5D229_HADSP	Q5D229 hadronyche
10	8	9.3	88	2 Q5D230_HADSP	Q5D230 hadronyche
11	8	9.3	90	2 Q5D233_HADIN	Q5D233 hadronyche
12	8	9.3	106	2 Q4RVU3_TETNG	Q4rvu3 tetraodon n
13	8	9.3	107	1 PROK2_RAT	Q8r413 rattus norv
14	8	9.3	107	2 Q5OE37_9MURI	Q5oe37 arvicanthis
15	8	9.3	107	2 Q5OE38_9MURI	Q5oe38 arvicanthis
16	8	9.3	108	2 Q6ISR0_HUMAN	Q6isr0 homo sapien
17	8	9.3	108	2 Q8G3H4_BOVIN	Q8g3h4 bos taurus
18	8	9.3	128	1 PROK2_MOUSE	Q9gxu7 mus musculus
19	8	9.3	128	2 Q8G3H5_BOVIN	Q8g3h5 bos taurus
20	8	9.3	128	2 Q5OE33_9MURI	Q5oe33 arvicanthis
21	8	9.3	128	2 Q5OE34_9MURI	Q5oe34 arvicanthis
22	8	9.3	128	2 Q6V8J7_RAT	Q6v8j7 rattus norv
23	8	9.3	129	1 PROK2_HUMAN	Q9hc23 homo sapien
24	8	9.3	129	2 Q53Z79_HUMAN	Q53z79 homo sapien
25	8	9.3	217	2 Q69BB6_CAMJE	Q69bb6 campylobact
26	8	9.3	217	2 Q4HD42_CAMCO	Q4hd42 campylobact
27	7	8.1	39	2 Q5OE61_9MURI	Q5oe61 arvicanthis
28	7	8.1	44	2 Q7R7M9_PLAYO	Q7r7m9 plasmodium
29	7	8.1	86	2 Q5OE35_9MURI	Q5oe35 arvicanthis
30	7	8.1	86	2 Q5OE36_9MURI	Q5oe36 arvicanthis
31	7	8.1	96	1 BV8_BONVA	Q9Pw66 bomblina var

RESULT 1
 ID PROK1_HUMAN STANDARD; PRT; 105 AA.
 AC P58294;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine).
 GN Name=PROK1; ORFNames=UNQ600/PRO1186;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21160229; PubMed=11259612;
 RA Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.-Y.;
 RT "Identification of two prokineticin cDNAs: recombinant proteins potentially contract gastrointestinal smooth muscle.";
 RL Mol. Pharmacol. 59:692-698(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;
 RA LeCouter J., Kowalski J., Foster J., Hass P., Zhang Z., Dillard-Telm L., Frantz G., Rangell L., DeGuzman L., Keller G.-A., Peale F., Gurney A., Hillan K.J., Ferrara N.;
 RT "Identification of an angiogenic mitogen selective for endocrine gland endothelium.";
 RL Nature 412:877-884(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX Fraser C.;
 RT "Mambakine, a snake venom related endocrine hormone that controls macrophages.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [5]

Q8JFQ0 bombina max
 Q5W280 bombina ori
 Q9GMT1 macaca fasc
 Q726W8 desulfovibr
 Q9F233 staphylococ
 P87219 candida alb
 Q5AIC3 candida alb
 Q607D6 methylococc
 Q72Y78 malloccybe s
 Q6TAS1 phanerocha
 Q4TQ18 erythroba
 Q6R7N8 phaecoallyb
 Q72816 inocybe gla
 Q7Z7Z7 inocybe que

ALIGNMENTS

[illegible]

Query Match 54.7%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVCGAGTCCCAISLWRLGRLMCTPLRGEGECPGSHK 47
Db 20 AVITGACERDVCGAGTCCCAISLWRLGRLMCTPLRGEGECPGSHK 66

RESULT 4
PROK1 RAT
ID PROK1 RAT STANDARD; PRT; 105 AA.
AC Q8R414;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VBGF).
DE growth factor) (EG-VBGF).
GN Name=Prok1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VBGF/prokineticins as cognate ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
CC -1- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the prokinectin family.

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DR EMBL; AY089983; AAM09104.1; -; mRNA.
DR HSSP; P25687; 1MT.
DR Ensembl; ENSRNOG0000018201; Rattus norvegicus.
DR RGD; 620898; Prok1.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0045765; P:regulation of angiogenesis; NAS.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
KW Growth factor; Mitogen; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 105 Prokineticin 1.
FT DISULFID 26 38 By similarity.
FT DISULFID 32 50 By similarity.
FT DISULFID 37 78 By similarity.
FT DISULFID 60 86 By similarity.
FT DISULFID 80 96 By similarity.
SQ SEQUENCE 105 AA; 11643 MW; 8DF0C42122B1C5B6 CRC64;

Query Match 33.7%; Score 29; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 6.7e-23;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVCGAGTCCCAISLWRLGLR 29
Db 20 AVITGACERDVCGAGTCCCAISLWRLGLR 48

RESULT 5
Q8K457 MOUSE
ID Q8K457 MOUSE PRELIMINARY; PRT; 81 AA.
AC Q8K457;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Prokineticin 1 (Fragment).
DE Name=Prok1; Synonyms=PK1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bernak J.C., Belluzzi J., Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
DR EMBL; AF487281; AAM49573.1; -; mRNA.
DR HSSP; P25687; 1MT.
DR Ensembl; ENSMUSG0000046213; Mus musculus.
DR MGI; MGI:2180370; Prok1.
DR GO; GO:0005576; C:extracellular region; IDA.
DR GO; GO:0000187; P:activation of MAPK; IDA.
DR GO; GO:0007623; P:circadian rhythm; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
FT NON TER 1
SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;

Query Match 20.9%; Score 18; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QCGAGTCCCAISLWRLGLR 29
Db 7 QCGAGTCCCAISLWRLGLR 24

RESULT 6
VPRA_DENPO
ID VPRA_DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Intestinal toxin 1 (Mamba intestinal toxin 1) (MIT 1) (MIT1) (Venom protein A).
DE Dendroaspis polylepsis polylepsis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OX NCBI_TaxID=8620;
RN [1]
RP PROTEIN SEQUENCE OF 1-80.
RC TISSUE=Venom;
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Strydom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis polylepsis polylepsis (black mamba) venom.";

RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
RN [2]
RP PROTEIN SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Venom;
RA MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RX Schweitz H., Pascaud P., Dicochet S., Moirier D., Lazdunski M.;
RA "MT1", a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RN FEBS Lett. 461:183-188(1998).
RP [3]
RP STRUCTURE BY NMR OF 1-81, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
RA Boissouvier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA Schweitz H., Lazdunski M., Marion D.;
RT "A structural homologue of colipase in black mamba venom revealed by
NMR floating disulphide bridge analysis.";
RL J. Mol. Biol. 283:205-219(1998).
CC -1- FUNCTION: Potently contracts gastrointestinal (GI) smooth muscle.
CC May act on potassium channels, but not on Kv1.1, Kv1.2, Kv1.3,
CC Kv1.4, Kv1.5, Kv2.1, Kv3.4, Kv4.2, TREK-1, HERG, KCNQ1, KCNQ2,
CC KCNQ3, IRK1, IRK2, ROMK1, GIRK1.2 and GIRK1.4.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the prokinectin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PDB: 1LMT; NMR: @=1-81.
KW 3D-structure; Direct protein sequencing; Toxin.
FT DISULFID 7 19
FT DISULFID 13 31
FT DISULFID 18 59
FT DISULFID 41 67
FT DISULFID 61 77
FT VARIANT 72 72 P -> Q (in protein A').
FT CONFLICT 18 18 C -> S (in Ref. 1).
FT CONFLICT 22 22 S -> C (in Ref. 1).
FT CONFLICT 54 54 R -> RK (in Ref. 1).
SQ SEQUENCE 81 AA; 8604 MW; 5F6B703434338B03 CRC64;

Query Match 11.6%; Score 10; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERD 10
Db 1 AVITGACERD 10
|||||

RESULT 7
Q4SR12 TETNG PRELIMINARY; PRT; 102 AA.
AC Q4SR12;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 11 SCAF14528, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG00014129001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontinae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouart V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAE01014528; CAF96920.1; -; Genomic_DNA.
DR NON_TER 102 102
SQ SEQUENCE 102 AA; 11062 MW; 470A2CDF2D069043 CRC64;

Query Match 11.6%; Score 10; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 HHTCPCLPNL 65
Db 89 HHTCPCLPNL 98
|||||

RESULT 8
Q5D228 HADSP PRELIMINARY; PRT; 88 AA.
AC Q5D228;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE ACTX-Hs20f7406 precursor (fragment).
OS Hadronyche sp. (strain 20) (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Hexathelidae; Hadronyche.
OX NCBI_TaxID=278061;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wilson D.T., Drinkwater R., Alewood P.F.;
RT "Molecules identified from the venom of Australian Funnel-web
RT spiders.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY914168; AAX11348.1; -; mRNA.
KW Signal.
FT SIGNAL <1 17 Potential.
FT CHAIN 18 88 ACTX-Hs20f7406.
FT NON_TER 1 1
SQ SEQUENCE 88 AA; 9596 MW; D60799EA05234994 CRC64;

Query Match 9.3%; Score 8; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CGAGTCCA 20
Db 25 CGAGTCCA 32
|||||

RESULT 9
Q5D229 HADSP PRELIMINARY; PRT; 88 AA.
AC Q5D229;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
 DE ACTX-Hs20f7418 precursor (Fragment).
 OS Hadronyche sp. (strain 20) (Funnel-web spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_TaxID=278061;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson D.T., Drinkwater R., Alewood P.F.;
 RT "Molecules identified from the venom of Australian Funnel-web
 spiders.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY914167; AAX11347.1; -; mRNA.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 1 Potential.
 FT NON_TER 1 1
 SQ SEQUENCE 88 AA; 9608 MW; D60799F3E14EE6AB CRC64;

Query Match 9.3%; Score 8; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGAGTCCA 20
 DB 25 CGAGTCCA 32

RESULT 10
 Q5D230 HADSP PRELIMINARY; PRT; 88 AA.
 AC Q5D230
 DT 10-MAY-2005 (Tremblrel. 30, Created)
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
 DE ACTX-Hs20f7390 precursor (Fragment).
 OS Hadronyche sp. (strain 20) (Funnel-web spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.
 OX NCBI_TaxID=278061;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson D.T., Drinkwater R., Alewood P.F.;
 RT "Molecules identified from the venom of Australian Funnel-web
 spiders.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY914166; AAX11346.1; -; mRNA.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 1 Potential.
 FT NON_TER 1 1
 SQ SEQUENCE 88 AA; 9580 MW; D60799F3E2BD2994 CRC64;

Query Match 9.3%; Score 8; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGAGTCCA 20
 DB 25 CGAGTCCA 32

RESULT 11
 Q5D233 HADIN PRELIMINARY; PRT; 90 AA.
 AC Q5D233
 DT 10-MAY-2005 (Tremblrel. 30, Created)
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
 DE ACTX-Hi:OBf7512 precursor.
 OS Hadronyche infensa (Fraser island funnel-web spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Hexathelidae; Hadronyche.

OX NCBI_TaxID=153481;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson D.T., Drinkwater R., Alewood P.F.;
 RT "Molecules identified from the venom of Australian Funnel-web
 spiders.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY914163; AAX11343.1; -; mRNA.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 18 Potential.
 FT NON_TER 25 90
 SQ SEQUENCE 90 AA; 9956 MW; 78F727C78648D20D CRC64;

Query Match 9.3%; Score 8; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CGAGTCCA 20
 DB 26 CGAGTCCA 33

RESULT 12
 Q4RVU3 TETNG PRELIMINARY; PRT; 106 AA.
 AC Q4RVU3
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
 DE Chromosome 9 SCAF14991, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00028169001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Bessat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthonard V., Jubin C., Castellani L., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN (2)

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CAAB01014991; CAG07489.1; -; Genomic_DNA.
 DR NON_TER 106 106
 SQ SEQUENCE 106 AA; 12098 MW; 8DA4DC1B388B3052 CRC64;

Query Match 9.3%; Score 8; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 HHTCPCLP 63
 DB 76 HHTCPCLP 83

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RESULT 13
PROK2_RAT
ID PROK2_RAT STANDARD; PRT; 107 AA.
AC QBR413;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Prokineticin 2 precursor (PK2).
GN Name=Prok2; Synonyms=Bv8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VEGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN [2]
RP EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX MEDLINE=2202134; PubMed=12034206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
CC -1- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC -1- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2) (Probable).
CC -1- SIMILARITY: Belongs to the prokineticin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY089984; AAM09105.1; -; mRNA.
DR HSSP; P25687; IIMT.
DR Ensembl; ENSRNOG0000010898; Rattus norvegicus.
DR RGD; 620280; Bv8.
DR GO; GO:0001664; F:G-protein-coupled receptor binding; IDA.
DR InterPro; IPR009523; Prokineticin.
DR PANTHER; PTHR18821; Prokineticin; 1.
DR Pfam; PF06607; Prokineticin; 1.
DR KEGG; Biological rhythms; Neuropeptide; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 107 Prokineticin 2.
FT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 85 By similarity.
FT DISULFID 67 93 By similarity.
FT DISULFID 87 103 By similarity.
SQ SEQUENCE 107 AA; 11594 MW; BDFE316DCB5FED0 CRC64;

Query Match 9.3%; Score 8; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 HHTCPCLP 63
DB 82 HHTCPCLP 89

RESULT 14
Q50E37_9MURI
ID Q50E37_9MURI PRELIMINARY; PRT; 107 AA.
AC Q50E37;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Prokineticin 2 variant 1S/2/4.
GN Name=Prok2;
OS Arvicanthus niloticus (African grass rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Arvicanthus.
OX NCBI_TaxID=61156;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15851527; DOI=10.1177/0748730405275135;
RA Lambert C.M., Machida K.K., Smale L., Nunez A.A., Weaver D.R.;
RT "Analysis of the Prokineticin 2 System in a Diurnal Rodent, the
RT Unstriped Nile Grass Rat (Arvicanthus niloticus).";
RL J. Biol. Rhythms 20:206-218(2005).
DR EMBL; AY820155; AAV73830.1; -; mRNA.
SQ SEQUENCE 107 AA; 11597 MW; CFAE8947354361BB CRC64;

Query Match 9.3%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 HHTCPCLP 63
DB 82 HHTCPCLP 89

RESULT 15
Q50E38_9MURI
ID Q50E38_9MURI PRELIMINARY; PRT; 107 AA.
AC Q50E38;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Prokineticin 2 variant 1A/2/4.
GN Name=Prok2;
OS Arvicanthus niloticus (African grass rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Arvicanthus.
OX NCBI_TaxID=61156;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15851527; DOI=10.1177/0748730405275135;
RA Lambert C.M., Machida K.K., Smale L., Nunez A.A., Weaver D.R.;
RT "Analysis of the Prokineticin 2 System in a Diurnal Rodent, the
RT Unstriped Nile Grass Rat (Arvicanthus niloticus).";
RL J. Biol. Rhythms 20:206-218(2005).
DR EMBL; AY820154; AAV73830.1; -; mRNA.
SQ SEQUENCE 107 AA; 11581 MW; DDBDBB472B5C8045 CRC64;

Query Match 9.3%; Score 8; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 HHTCPCLP 63
DB 82 HHTCPCLP 89

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Search completed: April 17, 2006, 15:31:32
Job time : 239 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2006, 15:44:10 ; Search time 26 Seconds
(without alignments)
140.541 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105

Perfect score: 86
Sequence: 1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 217505 seqs, 42489236 residues

Word size : 1

Total number of hits satisfying chosen parameters: 217385

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New.*
1: /SIDSS/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
5: /SIDSS/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /SIDSS/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	86	7	US-11-073-420-11
2	86	100.0	105	6	US-10-131-826A-470
3	86	100.0	105	6	US-10-973-115B-470
4	86	100.0	105	6	US-10-218-784-166
5	86	100.0	105	6	US-10-219-061-166
6	86	100.0	105	6	US-10-219-062-166
7	86	100.0	105	6	US-10-219-064-166
8	86	100.0	105	6	US-10-233-134-166
9	86	100.0	105	7	US-11-290-153-470
10	61	70.9	105	7	US-11-073-420-28
11	51	59.3	81	7	US-11-073-420-16
12	47	54.7	105	6	US-10-475-075-194
13	40	46.5	86	7	US-11-073-420-17
14	38	44.2	105	6	US-10-475-075-193
15	38	44.2	105	6	US-10-475-075-477
16	38	44.2	105	7	US-11-073-420-31
17	18	20.9	86	7	US-11-073-420-12
18	10	11.6	80	7	US-11-073-420-15
19	8	9.3	80	7	US-11-073-420-10
20	8	9.3	81	7	US-11-073-420-9
21	8	9.3	81	7	US-11-073-420-37
22	8	9.3	108	7	US-11-073-420-6
23	7	8.1	75	7	US-11-073-420-13
24	7	8.1	77	7	US-11-073-420-14
25	7	8.1	311	7	US-11-167-856-4

26 7 8.1 386 7 US-11-096-568A-18600 Sequence 18600, A
27 7 8.1 428 7 US-11-172-740-754 Sequence 754, App
28 7 8.1 428 7 US-11-188-298-2195 Sequence 2195, App
29 7 8.1 432 7 US-11-172-740-757 Sequence 757, App
30 7 8.1 432 7 US-11-188-298-12384 Sequence 12384, A
31 7 8.1 432 7 US-11-188-298-13959 Sequence 13959, A
32 7 8.1 4440 6 US-10-194-487-525 Sequence 525, App
33 7 8.1 4440 6 US-10-195-888-525 Sequence 525, App
34 7 8.1 4440 6 US-10-195-888-525 Sequence 525, App
35 7 8.1 4440 6 US-10-195-889-525 Sequence 525, App
36 6 7.0 40 6 US-10-895-861-32 Sequence 32, Appl
37 6 7.0 57 6 US-10-517-784-2 Sequence 2, Appl
38 6 7.0 133 6 US-10-667-295-221 Sequence 221, App
39 6 7.0 152 7 US-11-188-298-19593 Sequence 19593, A
40 6 7.0 166 7 US-11-072-512-2085 Sequence 2085, App
41 6 7.0 179 7 US-11-079-463-10183 Sequence 10183, A
42 6 7.0 205 6 US-10-453-372-762 Sequence 762, App
43 6 7.0 229 6 US-10-506-454-982 Sequence 982, App
44 6 7.0 245 6 US-10-131-826A-214 Sequence 214, App
45 6 7.0 245 6 US-10-973-115B-214 Sequence 214, App

ALIGNMENTS

RESULT 1
US-11-073-420-11
; Sequence 11, Application US/11073420
; Publication No. US20060019338A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Primate Prokineticin and Prokineticin
; TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods
; FILE REFERENCE: UC11210-1
; CURRENT APPLICATION NUMBER: US/11/073,420
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,753
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-420-11

Query Match 100.0%; Score 86; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.1e-87;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCAISLWLRGURMCTPLRGEGECHPGSHKVPFFPRKRKHHTCP 60
Db 1 AVITGACERDVQCGAGTCCAISLWLRGURMCTPLRGEGECHPGSHKVPFFPRKRKHHTCP 60
QY 61 CLPNLLCSRRFPDGRYRCMDLKNINF 86
Db 61 CLPNLLCSRRFPDGRYRCMDLKNINF 86

RESULT 2
US-10-131-826A-470
; Sequence 470, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

;
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR FILING DATE: 1998-08-10
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; PRIOR FILING DATE: 1998-08-31
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; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR APPLICATION NUMBER: 60/125259
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; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
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; PRIOR FILING DATE: 1999-03-29
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723

RESULT 5
US-10-219-061-166
Sequence 166, Application US/10219061
Publication No. US20060074224A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C16
CURRENT APPLICATION NUMBER: US/10/219,061
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17

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RESULT 6
US-10-219-062-166
Sequence 166, Application US/10219062
Publication No. US20060074220A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRAN
FILE REFERENCE: F3530P1C17
CURRENT APPLICATION NUMBER: US/10/21
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data rem
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 166

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; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-062-166

Query Match      100.0%; Score 86; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.9e-87;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGECHPGSHKVPFFFRKRKHTCP 79

QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
DB 80 CLPNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 7
US-10-219-064-166
; Sequence 166, Application US/10219064
; Publication No. US20060074221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC44
; CURRENT APPLICATION NUMBER: US/10/219,064
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 166
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-064-166

Query Match      100.0%; Score 86; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.9e-87;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGECHPGSHKVPFFFRKRKHTCP 60
DB 20 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGECHPGSHKVPFFFRKRKHTCP 60

QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
DB 80 CLPNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 8
US-10-233-134-166
; Sequence 166, Application US/10233134
; Publication No. US20060073476A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC113
; CURRENT APPLICATION NUMBER: US/10/233,134
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 166
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-233-134-166

Query Match      100.0%; Score 86; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.9e-87;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGECHPGSHKVPFFFRKRKHTCP 60
DB 20 AVITGACERDVQCGAGTCCCAISLWLRLGRLMCTPLRGEGECHPGSHKVPFFFRKRKHTCP 79

QY 61 CLPNLLCSRFPDGRYRCSDMLKNINF 86
DB 80 CLPNLLCSRFPDGRYRCSDMLKNINF 105

RESULT 9
US-11-290-153-470
; Sequence 470, Application US/11290153
; Publication No. US20060073568A1
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; FILE REFERENCE: UC11210-1
; CURRENT APPLICATION NUMBER: US/11/073,420
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,753
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Macaca mulatta
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-11-073-420-28

Query Match          70.9%; Score 61; DB 7; Length 105;
Best Local Similarity 100.0%; Pred.No.1.3e-59;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AVITGACERDVQCGAGTCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 60
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Db      20  AVITGACERDVQCGAGTCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFRKRKHHTCP 79

Qy      61 C 61
      ||
Db      80 C 80

RESULT 11
US-11-073-420-16
; Sequence 16, Application US/11073420
; Publication No. US20060019338A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: Primate Prokineticin and Prokineticin
; TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods
; FILE REFERENCE: UC11210-1
; CURRENT APPLICATION NUMBER: US/11/073,420
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 60/550,753
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-420-16

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Query Match      59.3%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 9,6e-49;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 AVITGACERDVQCAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFF 51
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Db   1 AVITGACERDVQCAGTCCCAISLWLRLGRLMCTPLGREGECHPGSHKVPFF 51
      |||||

RESULT 12
US-10-475-075-194

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; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 194
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 7.20796835452081
; OTHER INFORMATION: seq VSMILLVTVSDC/AV
US-10-475-075-194

Query Match 54.7%; Score 47; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.9e-44;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLRGEGECHPGSHK 47
Db 20 AVITGACERDVQCGAGTCCAIISLWRLGRLMCTPLRGEGECHPGSHK 66

RESULT 13
US-11-073-420-17
; Sequence 17, Application US/11073420
; Publication No. US20060019338A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Primate Prokineticin and Prokineticin
; FILE REFERENCE: UC11210-1
; CURRENT APPLICATION NUMBER: US/11/073,420
; PRIOR APPLICATION NUMBER: 2003-03-04
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-420-17

Query Match 46.5%; Score 40; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.2e-36;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 47 KVPFRKRKHTCPCLPNLLCSRFDPDGRYRCSDMLKNINF 86
Db 47 KVPFRKRKHTCPCLPNLLCSRFDPDGRYRCSDMLKNINF 86

RESULT 14
US-10-475-075-193
; Sequence 193, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18

; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 193
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 7.20796835452081
; OTHER INFORMATION: seq VSMILLVTVSDC/AV
; NAME/KEY: unsure
; LOCATION: 37
; OTHER INFORMATION: Xaa = Glu or *
US-10-475-075-193

Query Match 44.2%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 PFFRKRKHTCPCLPNLLCSRFDPDGRYRCSDMLKNINF 86
Db 68 PFFRKRKHTCPCLPNLLCSRFDPDGRYRCSDMLKNINF 105

RESULT 15
US-10-475-075-477
; Sequence 477, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 477
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; NAME/KEY: UNSURE
; LOCATION: 37
; OTHER INFORMATION: Xaa = Lys or *
US-10-475-075-477

Query Match 44.2%; Score 38; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 PFFRKRKHTCPCLPNLLCSRFDPDGRYRCSDMLKNINF 86
Db 68 PFFRKRKHTCPCLPNLLCSRFDPDGRYRCSDMLKNINF 105

Search completed: April 17, 2006, 15:47:18
Job time : 26 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 17, 2006, 15:27:50 ; Search time 38 Seconds
(without alignments)
217.754 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 86
Sequence: 1 AVITCAGRDVQCGAGTCCA.....CSRFPDGRYCRSMDLKNINF 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	8.1	587	2 AC1510	internalin protein
2	7	8.1	589	2 AB1151	internalin protein
3	7	8.1	759	2 E81869	probable ATP-depen
4	7	8.1	1345	2 B71608	DNA-directed RNA p
5	6	7.0	34	2 S10378	albumin (clone PHA
6	6	7.0	41	2 S10375	albumin (clone PHA
7	6	7.0	51	2 G82666	hypothetical prote
8	6	7.0	53	2 A90599	hypothetical prote
9	6	7.0	83	2 T36350	probable regulator
10	6	7.0	87	2 E64006	hypothetical prote
11	6	7.0	95	2 AD1168	hypothetical prote
12	6	7.0	104	2 T14868	excinuclease ABC c
13	6	7.0	113	2 S11532	colicin E1 immunit
14	6	7.0	114	2 I38286	T cell leukemia/ly
15	6	7.0	117	2 I57454	MHC class I antige
16	6	7.0	118	2 B80999	transcription fact
17	6	7.0	127	2 G90262	transcriptional re
18	6	7.0	128	2 B86693	hypothetical prote
19	6	7.0	140	2 S74072	hypothetical prote
20	6	7.0	156	2 T48047	hypothetical prote
21	6	7.0	167	1 S32716	ribosome releasing
22	6	7.0	172	2 A22606	acetyltransferase
23	6	7.0	172	2 E97388	hypothetical prote
24	6	7.0	190	2 B83990	hypothetical prote
25	6	7.0	217	1 BVH1XA	capsulation protei
26	6	7.0	217	2 A98196	hypothetical prote
27	6	7.0	219	2 H85358	hypothetical prote
28	6	7.0	225	2 A86043	probable transposa
29	6	7.0	227	2 T12549	hypothetical prote

30	6	7.0	229	2 H64367	dolichyl-phosphate
31	6	7.0	235	2 I68700	MHC HLA-A cell sur
32	6	7.0	236	2 E84255	hypothetical prote
33	6	7.0	238	2 I68699	MHC HLA-A cell sur
34	6	7.0	239	2 E95888	probable transcript
35	6	7.0	240	2 A95952	probable 2-deoxygl
36	6	7.0	243	2 B98199	ribitol 2-dehydrog
37	6	7.0	243	2 AG3087	ribitol 2-dehydrog
38	6	7.0	247	2 F84210	oxidoreductase hom
39	6	7.0	247	2 T00107	ABC-type transport
40	6	7.0	248	2 T44932	3-oxoacyl-(acyl-ca
41	6	7.0	249	2 A13156	short-chain dehydr
42	6	7.0	249	2 H98130	probable short-cha
43	6	7.0	255	2 AE0537	hypothetical prote
44	6	7.0	257	2 S23485	1,6-dihydroxycyclo
45	6	7.0	259	2 G95890	probable transcript

ALIGNMENTS

RESULT 1

AC1510
internalin protein, probable peptidoglycan bound protein (LPXTG motif) homolog lin0619
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AC1510
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <GLA>
A:Cross-references: UNIPROT:Q92B42; UNIPARC:UPI00000CC2C2; GB:AL592022; PIDN:CAC95851.1,
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0619

Query Match 8.1%; Score 7; DB 2; Length 587;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 FFRKRXKH 56
| | | | |
Db 580 FFRKRXKH 586

RESULT 2

AB1151
internalin proteins, probable peptidoglycan bound protein (LPXTG motif) homolog lmo0610
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1151
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1151
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-589 <GLA>
A:Cross-references: UNIPROT:Q8Y9C2; UNIPARC:UPI0000054C9D; GB:NC_003210; PIDN:CAC98688.1
A:Experimental source: strain EGD-e

C;Genetics:
A;Gene: lmo0610

Query Match 8.1%; Score 7; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 FFRKRXH 56
|||||
Db 582 FFRKRXH 588

RESULT 3
E81869
probable ATP-dependent proteinase ATP-binding protein NMA1045 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: E81869
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holozyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81869
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-759 <PAR>
A;Cross-references: UNIPROT:Q9JVL5; UNIPARC:UPI00000C4AE0; GB:AL162755; GB:AL157959; NID:10761919
A;Experimental source: serogroup A, strain Z2491
C;Genetics:

A;Gene: NMA1040; NMA1045
C;Superfamily: endopeptidase Clp ATP-binding chain
C;Keywords: ATP; molecular chaperone; nucleotide binding; P-loop
F;215-222/Region: nucleotide-binding motif A (P-loop)
F;282-287/Region: nucleotide-binding motif B
F;496-503/Region: nucleotide-binding motif A (P-loop)
F;561-566/Region: nucleotide-binding motif B
F;221/Binding site: ATP (Lys) #status predicted
F;502/Binding site: ATP (Lys) #status predicted

Query Match 8.1%; Score 7; DB 2; Length 759;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 LGREGEE 40
|||||
Db 156 LGREGEE 162

RESULT 4
B71608
DNA-directed RNA polymerase (EC 2.7.7.6) II second largest chain - malaria parasite (Plasmodium falciparum)
N;Alternate names: protein PFB0715W
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: B71608
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: B71608
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1345 <GAR>
A;Cross-references: UNIPROT:O96236; UNIPARC:UPI0000175764; GB:AE001413; GB:AE001362; NID:10761919
A;Experimental source: clone 3D7
C;Genetics:

A;Gene: PFB0715W
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription

Query Match 8.1%; Score 7; DB 2; Length 1345;

Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TPLGREG 38
|||||
Db 511 TPLGREG 517

RESULT 5
S10378
albumin (clone PHA1/PHA12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: S10378; S10377
R;Dmitrenko, V.V.; Kavasani, V.M.
submitted to the EMBL Data Library, January 1990
A;Description: Polyadenylation site heterogeneity of the mRNA for human serum albumin.
A;Reference number: S10375
A;Accession: S10378
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-34 <DMT>
A;Cross-references: UNIPROT:Q16885; UNIPARC:UPI0000073D0F; EMBL:X51363; NID:935452; PID:10761919
A;Accession: S10377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-32 <DM2>
A;Cross-references: UNIPARC:UPI000016AEA3; EMBL:X51364; NID:935453; PID:9930103
C;Keywords: plasma

Query Match 7.0%; Score 6; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 LKNINF 86
|||||
Db 10 LKNINF 15

RESULT 6
S10375
albumin (clone PHA19) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S10375
R;Dmitrenko, V.V.; Kavasani, V.M.
submitted to the EMBL Data Library, January 1990
A;Description: Polyadenylation site heterogeneity of the mRNA for human serum albumin.
A;Reference number: S10375
A;Accession: S10375
A;Molecule type: mRNA
A;Residues: 1-41 <DMT>
A;Cross-references: UNIPROT:Q14551; UNIPARC:UPI000017C070; EMBL:X51365
C;Keywords: plasma

Query Match 7.0%; Score 6; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 LKNINF 86
|||||
Db 20 LKNINF 25

RESULT 7
G82666
hypothetical protein XF1556 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82666
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: G82866
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-51 <SIM>
 A;Cross-references: UNIPROT:Q9PD23; UNIPARC:UPI00000C277C; GB:AE003985; GB:AE003849; NID
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
 as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XP1556

Query Match 7.0%; Score 6; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TPLGRE 37
 |||||
 DB 39 TPLGRE 44

RESULT 8
 A90599
 hypothetical protein MYPV_6970 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C;Species: Mycoplasma pulmonis
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 A;Accession: A90599
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: A90599
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-53 <KUR>
 A;Cross-references: UNIPROT:Q98PM5; UNIPARC:UPI00000C80F2; GB:AL445566; PID:g14090112; F
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPV 6970
 A;Genetic code: SGC3

Query Match 7.0%; Score 6; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 LKNINF 86
 |||||
 DB 17 LKNINF 22

RESULT 9
 T36350
 probable regulator - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 A;Accession: T36350
 R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, May 1999
 A;Reference number: Z21575
 A;Accession: T36350

A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-83 <OLI>
 A;Cross-references: UNIPROT:Q9X8K3; UNIPARC:UPI00000DB092; EMBL:AL049841; PIDN:CAB42777
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOEDB:SCE9.31c

Query Match 7.0%; Score 6; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 SRPFDG 73
 |||||
 DB 50 SRPFDG 55

RESULT 10
 E64006
 hypothetical protein H10326 - Haemophilus influenzae (strain Rd KW20)
 C;Species: Haemophilus influenzae
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 A;Accession: E64006
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
 Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A;Reference number: A64000; MUID:95350630; PMID:7542800
 A;Accession: E64006
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-87 <TIGR>
 A;Cross-references: UNIPROT:P43987; UNIPARC:UPI0000139622; GB:U32717; GB:LA2023; NID:g1

Query Match 7.0%; Score 6; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 VPFFRK 53
 |||||
 DB 81 VPFFRK 86

RESULT 11
 AD1168
 hypothetical protein lmo0748 [imported] - Listeria monocytogenes (strain EGD-e)
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 A;Accession: AD1168
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mo
 ok, C.; Schluerer, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AD1168
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-95 <GLA>
 A;Cross-references: UNIPROT:Q8Y8Z4; UNIPARC:UPI0000054D4F; GB:NC_003210; PIDN:CAC98826.1

Query Match 7.0%; Score 6; DB 2; Length 95;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 FFRKPK 55

Db 86 FFRK RK 91
|||||

RESULT 12

T14868
exonuclease ABC chain A uvra [similarity] - Salmonella typhimurium (fragment)
N;Contains: excision endonuclease ABC (EC 3.1.-.-) chain A
C;Species: Salmonella typhimurium
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14868
R;Wong, K.K.; McClelland, M.; Stillwell, L.C.; Sisk, E.C.; Thurston, S.J.; Safer, J.D.
Infect. Immun. 66, 3365-3371, 1998
A;Title: Identification and sequence analysis of a 27-kilobase chromosomal fragment containing typhimurium LT2.
A;Reference number: 218249; MUID:98298059; PMID:9632606
A;Accession: T14868
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-104 <WON>
A;Cross-references: UNIPROT:O85309; UNIPARC:UPI00000AF1CA; EMBL:AF060869; NID:g33233584;
C;Genetics:
A;Gene: uvra

A;Map position: 92 min
A;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
C;Keywords: ATP; DNA binding; DNA repair; hydrolase; nucleotide binding; P-loop
F;31-38/Region: nucleotide-binding motif A (P-loop)

Query Match 7.0%; Score 6; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 LKNINF 86
|||||
Db 14 LKNINF 19

RESULT 13

S11532
colicin E1 immunity protein - Shigella sonnei plasmid pKY-1
C;Species: Shigella sonnei
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: S11532
R;Higashi, M.; Hata, M.; Hase, T.; Yamaguchi, K.; Masamune, Y.
J. Gen. Appl. Microbiol. 32, 433-442, 1986
A;Title: The nucleotide sequence of cea and the region of origin of plasmid pKY-1.
A;Reference number: S06218
A;Accession: S11532
A;Molecule type: DNA
A;Residues: 1-113 <JGE>
A;Cross-references: UNIPROT:P22558; UNIPARC:UPI000012D622; EMBL:M37218; NID:g149346; PID
C;Genetics:
A;Gene: imm
A;Genome: plasmid
C;Superfamily: colicin E1 immunity protein

Query Match 7.0%; Score 6; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 FFRK RK 55
|||||
Db 69 FFRK RK 74

RESULT 14

I38286
T cell leukemia/lymphoma protein TCL1 - human
N;Alternate names: T-cell leukemia-related protein TCL1
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Oct-2004
C;Accession: I38286; S51138
R;Virgilio, L.; Narducci, M.G.; Isobe, M.; Billips, L.G.; Cooper, M.D.; Croce, C.M.; Rus

Proc. Natl. Acad. Sci. U.S.A. 91, 12530-12534, 1994
A;Title: Identification of the TCL1 gene involved in T-cell malignancies.
A;Reference number: I38286; MUID:95107991; PMID:7809072
A;Accession: I38286
A;Molecule type: mRNA
A;Residues: 1-114 <RES>
A;Cross-references: UNIPROT:P56279; UNIPARC:UPI00000413AD; EMBL:X82240; NID:g624960; PID
C;Genetics:
A;Gene: GDB:TCL1
A;Cross-references: GDB:250785
A;Map position: 14q32.1-14q32.1
C;Superfamily: T-cell leukemia/lymphoma protein 1A

Query Match 7.0%; Score 6; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 PDGRYR 76
|||||
Db 80 PDGRYR 85

RESULT 15

I57454
MHC class I antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I57454
R;Trowsdale, J.; Lee, J.; Kelly, A.; Carey, J.; Jenkins, J.; Travers, P.; Bodmer, W.F.
Mol. Biol. Med. 2, 53-61, 1984
A;Title: Isolation and sequencing of a cDNA clone for a human HLA-ABC antigen.
A;Reference number: I57454; MUID:85085508; PMID:6549041
A;Accession: I57454
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-117 <RES>
A;Cross-references: UNIPROT:O19689; UNIPARC:UPI0000089A5B; GB:M27971; NID:g187621; PID:
C;Genetics:
A;Gene: HLA-ABC
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 7.0%; Score 6; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGA 6
|||||
Db 72 AVITGA 77

Search completed: April 17, 2006, 15:32:17
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: April 17, 2006, 15:31:49 ; Search time 46 Seconds
(without alignments)
154.568 Million cell updates/sec

Title: US-10-027-603-2_COPY_20_105
Perfect score: 86
Sequence: 1 AVITGACERDVCGAGTCCA.....CSRFPDGRYRCMDLKNINF 86

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB pep.*
3: /cgn2_6/prodata/1/iaa/H COMB pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	105	2	US-09-712-529-5
2	86	100.0	105	2	US-10-212-201A-5
3	86	100.0	105	2	US-10-212-355-5
4	86	100.0	105	2	US-09-991-181-371
5	86	100.0	105	2	US-09-990-444-371
6	86	100.0	105	2	US-09-997-333-371
7	86	100.0	105	2	US-09-992-598-371
8	47	54.7	80	2	US-09-513-999C-4698
9	38	44.2	105	2	US-09-621-976-5350
10	8	9.3	108	2	US-09-712-529-2
11	8	9.3	108	2	US-10-212-201A-2
12	8	9.3	108	2	US-10-212-355-2
13	7	8.1	50	2	US-09-270-767-35963
14	7	8.1	50	2	US-09-270-767-51180
15	7	8.1	111	2	US-09-248-796A-16591
16	7	8.1	311	2	US-09-344-882-4
17	7	8.1	311	2	US-10-293-865-4
18	7	8.1	428	2	US-09-108-020-2
19	7	8.1	428	2	US-09-108-020-33
20	7	8.1	428	2	US-09-685-296-2
21	7	8.1	428	2	US-09-685-296-33
22	7	8.1	1345	1	US-08-977-767-3
23	7	8.1	3907	2	US-10-029-217A-24
24	6	7.0	19	2	US-10-009-962-12
25	6	7.0	19	2	US-10-671-628-12
26	6	7.0	23	2	US-09-062-440-13
27	6	7.0	23	2	US-09-712-495-13

ALIGNMENTS

RESULT 1
US-09-712-529-5
; Sequence 5, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-5

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; Sequence 5, Application US/10212201A				
; Patent No. 6756479				
; GENERAL INFORMATION:				
; APPLICANT: Sheppard, Paul O.				
; APPLICANT: Bishop, Paul D.				
; APPLICANT: Whitmore, Theodore E.				
; APPLICANT: Thompson, Penny P.				
; TITLE OF INVENTION: Human Zven Proteins				
; FILE REFERENCE: 99-81				
; CURRENT APPLICATION NUMBER: US/10/212,201A				
; CURRENT FILING DATE: 2002-08-02				
; PRIOR APPLICATION NUMBER: US/09/712,529				
; PRIOR FILING DATE: 2000-11-14				
; NUMBER OF SEQ ID NOS: 7				

Sequence 102, App
Sequence 39564, A
Sequence 54781, A
Sequence 13, Appl
Sequence 13, Appl
Sequence 53, Appl
Sequence 6668, Ap
Sequence 24565, A
Sequence 4, Appl
Sequence 11, Appl
Sequence 3231, Ap
Sequence 2, Appl
Sequence 2, Appl
Sequence 58247, A
Sequence 8076, Ap
Sequence 23103, A
Sequence 2810, Ap
Sequence 21, Appl

28 6 7.0 25 2 US-09-701-947A-102
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35 6 7.0 74 2 US-09-248-796A-24565
36 6 7.0 106 2 US-09-087-031E-11
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38 6 7.0 113 1 US-08-330-272-2
39 6 7.0 113 4 PCT-US95-13663-2
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41 6 7.0 129 2 US-09-543-681A-8076
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Db 20 AVITGACRDVQCGAGTCCALSMLRGLRMCTPLGREGECHPGSHKVPFFRKHKHTCP 79

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; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
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; ORGANISM: Homo sapiens
US-10-212-355-5

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QY 61 CLPNLLCSRFDPGRYRCSDMLKINF 86
Db 80 CLPNLLCSRFDPGRYRCSDMLKINF 105

RESULT 4
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; Sequence 371, Application US/09991181
; Patent No. 691319
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 86; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.7e-85;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 AVITGACERDVQCGAGTCCATSLWLRGLRMCTPLRGEGEECHPGSHKVPFFRKRKHTCP 79
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DB 80 CLPNLCSRFDPGRYRCSMDLKNINF 105

RESULT 5
US-09-990-444-371
; Sequence 371, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PlC19
CURRENT FILING DATE: 2001-11-14
CURRENT APPLICATION NUMBER: US/09/990,444
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 86; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.7e-85;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 20 AVITGACERDVQCGAGTCAISLWLRGLRMCTPLGREGECHPGSHKVPFFFRKRKHHTCP 79

QY 61 CLPNLLCSRFDPGRYRCSDMLKNINF 86
DB 80 CLPNLLCSRFDPGRYRCSDMLKNINF 105

RESULT 6
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; Sequence 371, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC27
; CURRENT APPLICATION NUMBER: US/09/997,333
; PRIOR FILING DATE: 2001-11-15
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; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 86; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.7e-85; Mismatches 0; Indels 0; Gaps 0;
Matches 86; Conservative 0;

Qy 1 AVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGREGECHPGSHKVPFFRKRRHTCP 60
Db 20 AVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGREGECHPGSHKVPFFRKRRHTCP 79
Qy 61 CLPNLLCSRFPDGRYRCMDLKNINF 86
Db 80 CLPNLLCSRFPDGRYRCMDLKNINF 105

RESULT 7
US-09-992-598-371
; Sequence 371, Application US/09992598
; Patent NO. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Query Match 100.0%; Score 86; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.7e-85;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCATSLWLRGRLMCTPLGREGECHPGSHKHTCP 60
Db 20 AVITGACERDVQCGAGTCCATSLWLRGRLMCTPLGREGECHPGSHKHTCP 79
Qy 61 CLPNLCSRRFPDGRYRCMDLKNINF 86
Db 80 CLPNLCSRRFPDGRYRCMDLKNINF 105

RESULT 8
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 7.2
; OTHER INFORMATION: seq VSIMLLVTVSDC/AV
US-09-513-999C-4698

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Best Local Similarity 100.0%; Pred. No. 4.1e-43;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVITGACERDVQCGAGTCCATSLWLRGRLMCTPLGREGECHPGSHK 47
Db 20 AVITGACERDVQCGAGTCCATSLWLRGRLMCTPLGREGECHPGSHK 66

RESULT 9

US-09-621-976-5350
; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
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; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; NAME/KEY: UNSURE
; LOCATION: 38
; OTHER INFORMATION: Xaa = Ala,Gly
US-09-621-976-5350

Query Match 44.2%; Score 38; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 PFFRKRRKHTKPCCLPPLLCSRRFPDGRYRCMDLKNINF 86
Db 68 PFFRKRRKHTKPCCLPPLLCSRRFPDGRYRCMDLKNINF 105

RESULT 10

US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712.529
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-529-2

Query Match 9.3%; Score 8; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 HHTCPCCLP 63
Db 83 HHTCPCCLP 90

RESULT 11
US-10-212-201A-2

; Sequence 2, Application US/10212201A
; Patent No. 6756479
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,201A
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/09/712,529
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-201A-2

Query Match 9.3%; Score 8; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 HHTCPCLP 63
Db 83 HHTCPCLP 90
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RESULT 12
US-10-212-355-2
; Sequence 2, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-2

Query Match 9.3%; Score 8; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 HHTCPCLP 63
Db 83 HHTCPCLP 90
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RESULT 13
US-09-270-767-35963
; Sequence 35963, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35963

; LENGTH: 50
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35963

Query Match 8.1%; Score 7; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 PFRKRKH 56
Db 30 PFRKRKH 36
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RESULT 14
US-09-270-767-51180
; Sequence 51180, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7328-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51180
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-51180

Query Match 8.1%; Score 7; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 PFRKRKH 56
Db 30 PFRKRKH 36
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RESULT 15
US-09-248-796A-16591
; Sequence 16591, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16591
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16591

Query Match 8.1%; Score 7; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TPLGREG 38
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Db 71 TPLGREG 77

Search completed: April 17, 2006, 15:33:09
Job time : 47 secs